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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=4; day=13; hr=17; min=2; sec=7; ms=359; ]

=====

Application No: 10566409 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2009-03-20 18:24:37.386  
**Finished:** 2009-03-20 18:24:55.179  
**Elapsed:** 0 hr(s) 0 min(s) 17 sec(s) 793 ms  
**Total Warnings:** 631  
**Total Errors:** 9  
**No. of SeqIDs Defined:** 699  
**Actual SeqID Count:** 699

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)

**Input Set:**

**Output Set:**

**Started:** 2009-03-20 18:24:37.386  
**Finished:** 2009-03-20 18:24:55.179  
**Elapsed:** 0 hr(s) 0 min(s) 17 sec(s) 793 ms  
**Total Warnings:** 631  
**Total Errors:** 9  
**No. of SeqIDs Defined:** 699  
**Actual SeqID Count:** 699

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (201)
W 402	Undefined organism found in <213> in SEQ ID (202)
W 402	Undefined organism found in <213> in SEQ ID (203)
W 402	Undefined organism found in <213> in SEQ ID (204)
W 402	Undefined organism found in <213> in SEQ ID (205)
W 402	Undefined organism found in <213> in SEQ ID (206)
E 257	Invalid sequence data feature in <221> in SEQ ID (212)
E 257	Invalid sequence data feature in <221> in SEQ ID (216)
W 402	Undefined organism found in <213> in SEQ ID (451)
W 402	Undefined organism found in <213> in SEQ ID (452)
W 402	Undefined organism found in <213> in SEQ ID (457)
W 402	Undefined organism found in <213> in SEQ ID (458)
W 251	Found intentionally skipped sequence in SEQID (520 )
W 251	Found intentionally skipped sequence in SEQID (521 )
W 251	Found intentionally skipped sequence in SEQID (522 )
W 251	Found intentionally skipped sequence in SEQID (523 )
W 251	Found intentionally skipped sequence in SEQID (524 )
W 251	Found intentionally skipped sequence in SEQID (525 )
W 251	Found intentionally skipped sequence in SEQID (526 )
W 251	Found intentionally skipped sequence in SEQID (527 )
W 251	Found intentionally skipped sequence in SEQID (639 )

**Input Set:**

**Output Set:**

**Started:** 2009-03-20 18:24:37.386  
**Finished:** 2009-03-20 18:24:55.179  
**Elapsed:** 0 hr(s) 0 min(s) 17 sec(s) 793 ms  
**Total Warnings:** 631  
**Total Errors:** 9  
**No. of SeqIDs Defined:** 699  
**Actual SeqID Count:** 699

Error code	Error Description
W 251	Found intentionally skipped sequence in SEQID (640 )
W 251	Found intentionally skipped sequence in SEQID (643 )
W 251	Found intentionally skipped sequence in SEQID (646 )
W 251	Found intentionally skipped sequence in SEQID (680 )
W 251	Found intentionally skipped sequence in SEQID (681 )
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
W 251	Found intentionally skipped sequence in SEQID (699 )

<110> Ledbetter, Jeffrey A.  
Hayden-Ledbetter, Martha S.  
Thompson, Peter A.

<120> BINDING CONSTRUCTS AND METHODS FOR USE THEREOF

<130> 910180.40102USPC

<140> 10566409  
<141> 2009-03-20

<150> PCT/US2003/041600

<151> 2003-12-24

<150> US 10/627,556

<151> 2003-07-26

<150> US 10/053,530

<151> 2002-01-17

<150> US 60/367,358

<151> 2001-01-17

<160> 699

<170> PatentIn version 3.2

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<212> DNA  
<213> Homo sapiens  
<400> 1

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atctcccgga cccctgaggt cacatgcgtg gtgggtggacg tgagccacga agaccctgag	180
gtcaagttaa actggtaacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg	240
gaggagcagt acaacagcac gtaccgtgtg gtcagcgtcc tcaccgtcct gcaccaggac	300
tggctgaatg gcaaggagta caagtgcag gtctccaaca aagccctccc agccccatc	360
gagaaaacaa tctccaaagc caaaggcag ccccgagaac cacaggtgta caccctgccc	420
ccatcccgaa atgagctgac caagaaccag gtcagcctga cctgcctggt caaaggcttc	480
tatcccagcg acatgcgcgt ggagtggag agcaatgggc agccggagaa caactacaag	540
accacgcctc ccgtgctgga ctccgacggc tccttcttcc tctacagcaa gtcaccgtg	600
gacaagagca ggtggcagca ggggaacgtc ttctcatgtc ccgtgatgca tgaggcttg	660
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<210> 2

<211> 235

<212> PRT

<213> Homo sapiens

<400> 2

Ser Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro			
1	5	10	15
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro			
20	25	30	
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr			
35	40	45	

Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
50						55					60				
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
65					70					75					80
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
						85				90			95		
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
								100		105				110	
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
							115		120			125			
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
							130		135			140			
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
145						150				155					160
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
							165			170				175	
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
							180			185			190		
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
							195		200			205			
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
							210		215			220			
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
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<223> n is a, c, g, or t
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<223> n is a, c, g, or t
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actnccagga ggcccttctg tctttgtctt cccccggaaa cccaaggacg tcctctccat
tttqqaqgc cqagtcacgt qcgttqtagt qqacgtcqqa aaaaqaqacc ccqaggtcaa
60
120
180
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tttcaactgg tatattgatg	gcgtttaggt	gcgaacggcc	aatacgaagc	caaaagagga	240
acagttaaac	agcacgtacc	gcgtggctag	cgtcctgccc	atccagcacc	300
gacggggaaag	gaattcaagt	gcaaggtcaa	caacaaagct	ctcccgcccc	360
gaccatctcc	aaggccaaag	ggcagacccg	ggagccgcag	gtgtacaccc	420
ccgggaagaa	ctggccaagg	acaccgtgag	cgtAACATGC	ctggtaaaag	480
agctgacatc	aacgttgagt	ggcagaggaa	cggtcagccg	gagttagagg	540
caacacgccc	ccacagctgg	acaacgacgg	gacctacttc	ctctacagca	600
gggaaagaac	acgtggcagc	ggggagaaac	cttaacctgt	gtggtgatgc	660
gcacaaccac	tacacccaga	aatccatcac	ccagtcttcg	ggtaaatagt	718

<210> 4

<211> 231

<212> PRT

<213> Lama glama

<400> 4

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Pro	Gly	Gly	Pro	Ser	Val	Phe	Val	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val
	20														30
Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
	35														45
Gly	Lys	Glu	Asp	Pro	Glu	Val	Asn	Phe	Asn	Trp	Tyr	Ile	Asp	Gly	Val
	50														60
Glu	Val	Arg	Thr	Ala	Asn	Thr	Lys	Pro	Lys	Glu	Glu	Gln	Phe	Asn	Ser
	65														80
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu
	85														95
Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala
	100														110
Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu	Pro
	115														125
Gln	Val	Tyr	Thr	Leu	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	Lys	Asp	Thr
	130														140
Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ala	Asp	Ile	Asn
	145														160
Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	Thr	Tyr	Ala
	165														175
Asn	Thr	Pro	Pro	Gln	Leu	Asp	Asn	Asp	Gly	Thr	Tyr	Phe	Leu	Tyr	Ser
	180														190
Arg	Leu	Ser	Val	Gly	Lys	Asn	Thr	Trp	Gln	Arg	Gly	Glu	Thr	Leu	Thr
	195														205
Gly	Val	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
	210														220
Ile	Thr	Gln	Ser	Ser	Gly	Lys									
	225														230

<210> 5

<211> 757

<212> DNA

<213> Lama glama

<400> 5

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catttcccc	ccgaaaccca	aggacgtct	ctccatttct	gggaggcccc	aggtcacgtg	180
cgttgtggta	gacgtgggcc	aggaagaccc	cgaggtcagt	ttcaactgggt	acattgtatgg	240
cgcgtgggtg	cgaacggcca	acacgaggcc	aaaagaggaa	cagttcaaca	gcacgttaccg	300
cgttgtcagc	gtccctgcccc	tccagcacca	ggactggctg	acgggaaagg	aattcaagtg	360

caaggtaaac	aacaaagctc	tcccgcccc	catcgagaag	accatctcca	aggccaaagg	420
gcagacccgg	gagccgcagg	tgtacaccct	ggccccacac	cgggaagagc	tggccaagga	480
caccgtgagc	gtaacatgcc	tggtaaaagg	cttctaccca	cctgatatca	acgttgagtg	540
gcagaggaat	gggcagccgg	agttaggggg	cacytacgcc	accacgcccac	cccagctgga	600
caacgacggg	acctacttcc	tctacagcaa	gctctcggtg	gaaagaaca	cgtggcagca	660
gggagaaaacc	ttcacctgtg	tggtgatgca	cgaggccctg	cacaaccact	acacccagaa	720
atccatacc	cagtcttcgg	gtaaatagta	atctaga			757

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<213> Lama glama						
<400> 6						
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20	25		30			
Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp						
35	40		45			
Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp						
50	55		60			
Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly						
65	70		75		80	
Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn						
85	90		95			
Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp						
100	105		110			
Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro						
115	120		125			
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu						
130	135		140			
Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp						
145	150		155		160	
Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile						
165	170		175			
Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr						
180	185		190			
Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr						
195	200		205			
Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe						
210	215		220			
Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys						
225	230		235		240	
Ser Ile Thr Gln Ser Ser Gly Lys						
245						

<210> 7						
<211> 727						
<212> DNA						
<213> Lama glama						
<400> 7						
tgatcaagcg caccacagcg aagacccag ctccaagtgt cccaaatgcc caggccctga					60	
actccttggaa gggccacacgg tcttcatctt cccccccggaaa gccaaggacgc tcctctccat					120	
cacccggaaaa cctgagggtca cgtgcttgg gttggacgtgg gtaaagaaga ccctgagatc					180	
gagttcaagc tggccgtgg atgacacaga ggtacacacg gctgagacaa agccaaaggaa					240	
ggaacagttc aacagcacgt accgcgtgg cagcgtccctg cccatccagc accaggactg					300	
gctgacgggg aaggaattca agtgcacggt caacaacaaa gctctccctg ccccatcgaa					360	

gaggaccatc	tccaaggcca	aagggcagac	ccgggagccg	caggtgtaca	ccctggccc	420
acaccggaa	gagctggcca	aggacaccgt	gagcgttaacc	tgcctggta	aaggcttctt	480
cccagctgac	atcaacgttg	agtggcagag	gaatggcag	ccggagtcag	agggcaccta	540
cccaaacacg	ccgccacagc	tggacaacga	ccggacctac	ttcctctaca	gaaaactctc	600
cgtggaaag	aacacgtggc	agcagggaga	agtcttcacc	tgtgtggta	tgcacgagc	660
tctacacaat	cactccaccc	agaaatccat	cacccagtct	tcgggtaaat	agtaatctag	720
aggccc						727

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<212> PRT						
<213> Lama glama						
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Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro						
20 25 30						
Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys						
35 40 45						
Leu Trp Trp Thr Trp Val Lys Thr Leu Arg Ser Ser Ser Trp						
50 55 60						
Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu						
65 70 75 80						
Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln						
85 90 95						
His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn						
100 105 110						
Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly						
115 120 125						
Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu						
130 135 140						
Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe						
145 150 155 160						
Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser						
165 170 175						
Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr						
180 185 190						
Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln						
195 200 205						
Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His						
210 215 220						
Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys						
225 230 235						

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<211> 18						
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<213> Homo sapiens						
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1	5	10	15		
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<211> 54					
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<213> Homo sapiens					
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agca					
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<211> 18					
<212> PRT					
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<400> 12					
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1	5	10	15		
Pro Ala					
<210> 13					
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<212> DNA					
<213> Homo sapiens					
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gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg					180
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag					240
gactggctga atggcaagga gtacaagtgc aaggcttcca acaaagccct cccagccccc					300
atcgagaaaa ccatctccaa agccaaa					327
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<213> Homo sapiens					
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Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val					
20	25	30			
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val					
35	40	45			
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln					
50	55	60			
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln					
65	70	75	80		
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala					
85	90	95			
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys					
100	105				
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<213> Homo sapiens					
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 tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc 180  
 gacggctcct tcttcctcta tagcaagctc accgtggaca agagcaggtg gcagcagggg 240  
 aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 300  
 ctctccctgt ccccggttaa atga 324

<210> 16  
 <211> 107  
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 <213> Homo sapiens  
 <400> 16

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1				5					10				15		
Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
									20			25		30	
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
							35		40			45			
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
							50		55			60			
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
							65		70			75		80	
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
							85		90			95			
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
							100		105						

<210> 17  
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 <212> DNA  
 <213> Homo sapiens  
 <400> 17

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<210> 18  
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 <212> PRT  
 <213> Homo sapiens  
 <400> 18

Asp	Gln	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser
1				5					10				15		
Pro	Ala														

<210> 19  
 <211> 712  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Synthetic  
 nucleotide sequence

<400> 19

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